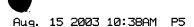
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AMENDMENT

In the Claims:

Cancel claims 61, 62, 63-68, 69, and 70-76 without prejudice.

Reiterated claims are as follows.

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- 37. (Reiterated) A transgenic plant comprising a recombinant polynucleotide encoding SEQ ID NO: 18, and said transgenic plant has enhanced tolerance to fungal disease due to expression of SEQ ID NO: 18.
- 39. (Reiterated) The transgenic plant of claim 37, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.
- 40. (Reiterated) The transgenic plant of claim 37, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.
- 41. (Reiterated) The transgenic plant of claim 40, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.
- 42. (Reiterated) The transgenic plant of claim 41, wherein said promoter is constitutive, inducible, or tissue-specific.
- 44. (Reiterated) The transgenic plant of claim 37, wherein said fungal disease is caused by Fusarium, Erysiphe, Sclerotinia or Botrytis.
- 45. (Reiterated) A method for enhancing the disease tolerance or resistance of a plant comprising transforming a plant with a recombinant polynucleotide encoding SEQ ID NO: 18, and said transgenic plant has enhanced tolerance to fungal disease due to expression of SEQ ID NO: 18.
- 47. (Reiterated) The method of claim 45, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.

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- 48. (Reiterated) The method of claim 45, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.
- 49. (Reiterated) The method of claim 48, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.
- 50. (Reiterated) The method of claim 49, wherein said promoter is constitutive, inducible, or tissue-specific.
- 52. (Reiterated) The transgenic plant of claim 45, wherein said fungal disease is caused by Fusarium, Erysiphe, Sclerotinia or Botrytis.
- 53. (Reiterated) A method for altering the expression levels of at least one gene in a plant comprising transforming the plant with a recombinant polynucleotide encoding SEQ ID NO: 18, and said transgenic plant has enhanced tolerance to fungal disease due to expression of SEQ ID NO: 18.
- 55. (Reiterated) The method of claim 53, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.
- 56. (Reiterated) The method of claim 53, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.
- 57. (Reiterated) The method of claim 56, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.
- 58. (Reiterated) The method of claim 57, wherein said promoter is constitutive, inducible, or tissue-specific.
- 60. (Reiterated) The transgenic plant of claim 53, wherein said fungal disease is caused by Fusarium, Erysiphe, Sclerotinia or Botrytis.